

## SEQUENCE LISTING

<110> Whitehead Institute for Biomedical Research  
Hug, Christopher  
Lodish, Harvey F.

<120> USE OF T-CADHERIN AS A TARGET

<130> SER-100X

<150> US 60/526,956

<151> 2003-12-03

<160> 18

<170> PatentIn version 3.1

<210> 1

<211> 713

<212> PRT

<213> Homo sapiens

<220>

<221> SIGNAL

<222> (1) .. (22)

<223>

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<221> LIPID

<222> (693) .. (693)

<223> GPI-ANCHOR

<220>

<221> PROPEP

<222> (23) .. (139)

<223>

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<221> PROPEP

<222> (694) .. (713)

<223>

<400> 1

Met Gln Pro Arg Thr Pro Leu Val Leu Cys Val Leu Leu Ser Gln Val  
1 5 10 15

Leu Leu Leu Thr Ser Ala Glu Asp Leu Asp Cys Thr Pro Gly Phe Gln  
20 25 30

Gln Lys Val Phe His Ile Asn Gln Pro Ala Glu Phe Ile Glu Asp Gln  
35 40 45

Ser Ile Leu Asn Leu Thr Phe Ser Asp Cys Lys Gly Asn Asp Lys Leu  
50 55 60

Arg Tyr Glu Val Ser Ser Pro Tyr Phe Lys Val Asn Ser Asp Gly Gly

65		70		75		80
Leu Val Ala Leu Arg Asn Ile Thr Ala Val Gly Lys Thr Leu Phe Val						
	85			90		95
His Ala Arg Thr Pro His Ala Glu Asp Met Ala Glu Leu Val Ile Val						
	100		105			110
Gly Gly Lys Asp Ile Gln Gly Ser Leu Gln Asp Ile Phe Lys Phe Ala						
	115		120			125
Arg Thr Ser Pro Val Pro Arg Gln Lys Arg Ser Ile Val Val Ser Pro						
	130		135		140	
Ile Leu Ile Pro Glu Asn Gln Arg Gln Pro Phe Pro Arg Asp Val Gly						
	145		150		155	160
Lys Val Val Asp Ser Asp Arg Pro Glu Arg Ser Lys Phe Arg Leu Thr						
	165		170			175
Gly Lys Gly Val Asp Gln Glu Pro Lys Gly Ile Phe Arg Ile Asn Glu						
	180		185			190
Asn Thr Gly Ser Val Ser Val Thr Arg Thr Leu Asp Arg Glu Val Ile						
	195		200		205	
Ala Val Tyr Gln Leu Phe Val Glu Thr Thr Asp Val Asn Gly Lys Thr						
	210		215		220	
Leu Glu Gly Pro Val Pro Leu Glu Val Ile Val Ile Asp Gln Asn Asp						
	225		230		235	240
Asn Arg Pro Ile Phe Arg Glu Gly Pro Tyr Ile Gly His Val Met Glu						
	245		250			255
Gly Ser Pro Thr Gly Thr Thr Val Met Arg Met Thr Ala Phe Asp Ala						
	260		265			270
Asp Asp Pro Ala Thr Asp Asn Ala Leu Leu Arg Tyr Asn Ile Arg Gln						
	275		280		285	
Gln Thr Pro Asp Lys Pro Ser Pro Asn Met Phe Tyr Ile Asp Pro Glu						
	290		295		300	
Lys Gly Asp Ile Val Thr Val Val Ser Pro Ala Leu Leu Asp Arg Glu						
	305		310		315	320
Thr Leu Glu Asn Pro Lys Tyr Glu Leu Ile Ile Glu Ala Gln Asp Met						
	325		330			335
Ala Gly Leu Asp Val Gly Leu Thr Gly Thr Ala Thr Ala Thr Ile Met						
	340		345			350
Ile Asp Asp Lys Asn Asp His Ser Pro Lys Phe Thr Lys Lys Glu Phe						
	355		360		365	
Gln Ala Thr Val Glu Glu Gly Ala Val Gly Val Ile Val Asn Leu Thr						
	370		375		380	

Val Glu Asp Lys Asp Asp Pro Thr Thr Gly Ala Trp Arg Ala Ala Tyr  
 385 390 395 400  
 Thr Ile Ile Asn Gly Asn Pro Gly Gln Ser Phe Glu Ile His Thr Asn  
 405 410 415  
 Pro Gln Thr Asn Glu Gly Met Leu Ser Val Val Lys Pro Leu Asp Tyr  
 420 425 430  
 Glu Ile Ser Ala Phe His Thr Leu Leu Ile Lys Val Glu Asn Glu Asp  
 435 440 445  
 Pro Leu Val Pro Asp Val Ser Tyr Gly Pro Ser Ser Thr Ala Thr Val  
 450 455 460  
 His Ile Thr Val Leu Asp Val Asn Glu Gly Pro Val Phe Tyr Pro Asp  
 465 470 475 480  
 Pro Met Met Val Thr Arg Gln Glu Asp Leu Ser Val Gly Ser Val Leu  
 485 490 495  
 Leu Thr Val Asn Ala Thr Asp Pro Asp Ser Leu Gln His Gln Thr Ile  
 500 505 510  
 Arg Tyr Ser Val Tyr Lys Asp Pro Ala Gly Trp Leu Asn Ile Asn Pro  
 515 520 525  
 Ile Asn Gly Thr Val Asp Thr Thr Ala Val Leu Asp Arg Glu Ser Pro  
 530 535 540  
 Phe Val Asp Asn Ser Val Tyr Thr Ala Leu Phe Leu Ala Ile Asp Ser  
 545 550 555 560  
 Gly Asn Pro Pro Ala Thr Gly Thr Gly Thr Leu Leu Ile Thr Leu Glu  
 565 570 575  
 Asp Val Asn Asp Asn Ala Pro Phe Ile Tyr Pro Thr Val Ala Glu Val  
 580 585 590  
 Cys Asp Asp Ala Lys Asn Leu Ser Val Val Ile Leu Gly Ala Ser Asp  
 595 600 605  
 Lys Asp Leu His Pro Asn Thr Asp Pro Phe Lys Phe Glu Ile His Lys  
 610 615 620  
 Gln Ala Val Pro Asp Lys Val Trp Lys Ile Ser Lys Ile Asn Asn Thr  
 625 630 635 640  
 His Ala Leu Val Ser Leu Leu Gln Asn Leu Asn Lys Ala Asn Tyr Asn  
 645 650 655  
 Leu Pro Ile Met Val Thr Asp Ser Gly Lys Pro Pro Met Thr Asn Ile  
 660 665 670  
 Thr Asp Leu Arg Val Gln Val Cys Ser Cys Arg Asn Ser Lys Val Asp  
 675 680 685

Cys Asn Ala Ala Gly Ala Leu Arg Phe Ser Leu Pro Ser Val Leu Leu  
 690 695 700

Leu Ser Leu Phe Ser Leu Ala Cys Leu  
 705 710

<210> 2  
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 <212> PRT  
 <213> Homo sapiens

<220>  
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 <222> (1)..(14)  
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 <222> (42)..(107)  
 <223> Collagen-like domain

<220>  
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 <222> (108)..(244)  
 <223> Clq domain

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Met Leu Leu Leu Gly Ala Val Leu Leu Leu Leu Ala Leu Pro Gly His  
 1 5 10 15

Asp Gln Glu Thr Thr Thr Gln Gly Pro Gly Val Leu Leu Pro Leu Pro  
 20 25 30

Lys Gly Ala Cys Thr Gly Trp Met Ala Gly Ile Pro Gly His Pro Gly  
 35 40 45

His Asn Gly Ala Pro Gly Arg Asp Gly Arg Asp Gly Thr Pro Gly Glu  
 50 55 60

Lys Gly Glu Lys Gly Asp Pro Gly Leu Ile Gly Pro Lys Gly Asp Ile  
 65 70 75 80

Gly Glu Thr Gly Val Pro Gly Ala Glu Gly Pro Arg Gly Phe Pro Gly  
 85 90 95

Ile Gln Gly Arg Lys Gly Glu Pro Gly Glu Gly Ala Tyr Val Tyr Arg  
 100 105 110

Ser Ala Phe Ser Val Gly Leu Glu Thr Tyr Val Thr Ile Pro Asn Met  
 115 120 125

Pro Ile Arg Phe Thr Lys Ile Phe Tyr Asn Gln Gln Asn His Tyr Asp  
 130 135 140

Gly Ser Thr Gly Lys Phe His Cys Asn Ile Pro Gly Leu Tyr Tyr Phe

145                      150                      155                      160  
 Ala Tyr His Ile Thr Val Tyr Met Lys Asp Val Lys Val Ser Leu Phe  
                                  165                      170                      175  
 Lys Lys Asp Lys Ala Met Leu Phe Thr Tyr Asp Gln Tyr Gln Glu Asn  
                                  180                      185                      190  
 Asn Val Asp Gln Ala Ser Gly Ser Val Leu Leu His Leu Glu Val Gly  
                                  195                      200                      205  
 Asp Gln Val Trp Leu Gln Val Tyr Gly Glu Gly Glu Arg Asn Gly Leu  
                                  210                      215                      220  
 Tyr Ala Asp Asn Asp Asn Asp Ser Thr Phe Thr Gly Phe Leu Leu Tyr  
                                  225                      230                      235                      240

His Asp Thr Asn

<210> 3  
 <211> 247  
 <212> PRT  
 <213> Mus musculus

<220>  
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 <222> (1)..(17)  
 <223>

<220>  
 <221> DOMAIN  
 <222> (45)..(110)  
 <223> Collagen-like domain

<220>  
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 <222> (111)..(247)  
 <223> Clq domain

<400> 3

Met Leu Leu Leu Gln Ala Leu Leu Phe Leu Leu Ile Leu Pro Ser His  
 1                      5                      10                      15  
 Ala Glu Asp Asp Val Thr Thr Thr Glu Glu Leu Ala Pro Ala Leu Val  
                                  20                      25                      30  
 Pro Pro Pro Lys Gly Thr Cys Ala Gly Trp Met Ala Gly Ile Pro Gly  
                                  35                      40                      45  
 His Pro Gly His Asn Gly Thr Pro Gly Arg Asp Gly Arg Asp Gly Thr  
                                  50                      55                      60  
 Pro Gly Glu Lys Gly Glu Lys Gly Asp Ala Gly Leu Leu Gly Pro Lys  
 65                      70                      75                      80  
 Gly Glu Thr Gly Asp Val Gly Met Thr Gly Ala Glu Gly Pro Arg Gly  
                                  85                      90                      95

Phe Pro Gly Thr Pro Gly Arg Lys Gly Glu Pro Gly Glu Ala Ala Tyr  
 100 105 110  
 Met Tyr Arg Ser Ala Phe Ser Val Gly Leu Glu Thr Arg Val Thr Val  
 115 120 125  
 Pro Asn Val Pro Ile Arg Phe Thr Lys Ile Phe Tyr Asn Gln Gln Asn  
 130 135 140  
 His Tyr Asp Gly Ser Thr Gly Lys Phe Tyr Cys Asn Ile Pro Gly Leu  
 145 150 155 160  
 Tyr Tyr Phe Ser Tyr His Ile Thr Val Tyr Met Lys Asp Val Lys Val  
 165 170 175  
 Ser Leu Phe Lys Lys Asp Lys Ala Val Leu Phe Thr Tyr Asp Gln Tyr  
 180 185 190  
 Gln Glu Lys Asn Val Asp Gln Ala Ser Gly Ser Val Leu Leu His Leu  
 195 200 205  
 Glu Val Gly Asp Gln Val Trp Leu Gln Val Tyr Gly Asp Gly Asp His  
 210 215 220  
 Asn Gly Leu Tyr Ala Asp Asn Val Asn Asp Ser Thr Phe Thr Gly Phe  
 225 230 235 240  
 Leu Leu Tyr His Asp Thr Asn  
 245

<210> 4  
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<220>  
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 <223> GPI-ANCHOR

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 <222> (694)..(714)  
 <223>

<400> 4

Met Gln Pro Arg Thr Pro Leu Thr Leu Cys Val Leu Leu Ser Gln Val  
 1 5 10 15  
 Leu Leu Val Thr Ser Ala Asp Asp Leu Glu Cys Thr Pro Gly Phe Gln  
 20 25 30  
 Arg Lys Val Leu His Ile His Gln Pro Ala Glu Phe Ile Glu Asp Gln  
 35 40 45  
 Pro Val Leu Asn Leu Thr Phe Asn Asp Cys Lys Gly Asn Glu Lys Leu  
 50 55 60  
 His Tyr Glu Val Ser Ser Pro His Phe Lys Val Asn Ser Asp Gly Thr  
 65 70 75 80  
 Leu Val Ala Leu Arg Asn Ile Thr Ala Val Gly Arg Thr Leu Phe Val  
 85 90 95  
 His Ala Arg Thr Pro His Ala Glu Asp Met Ala Glu Leu Val Ile Val  
 100 105 110  
 Gly Gly Lys Asp Ile Gln Gly Ser Leu Gln Asp Ile Phe Lys Phe Ala  
 115 120 125  
 Arg Thr Ser Pro Val Pro Arg Gln Lys Arg Ser Ile Val Val Ser Pro  
 130 135 140  
 Ile Leu Ile Pro Glu Asn Gln Arg Gln Pro Phe Pro Arg Asp Val Gly  
 145 150 155 160  
 Lys Val Val Asp Ser Asp Arg Pro Glu Gly Ser Lys Phe Arg Leu Thr  
 165 170 175  
 Gly Lys Gly Val Asp Gln Asp Pro Lys Gly Thr Phe Arg Ile Asn Glu  
 180 185 190  
 Asn Thr Gly Ser Val Ser Val Thr Arg Thr Leu Asp Arg Glu Thr Ile  
 195 200 205  
 Ala Thr Tyr Gln Leu Tyr Val Glu Thr Thr Asp Ala Ser Gly Lys Thr  
 210 215 220  
 Leu Glu Gly Pro Val Pro Leu Glu Val Ile Val Ile Asp Gln Asn Asp  
 225 230 235 240  
 Asn Arg Pro Ile Phe Arg Glu Gly Pro Tyr Ile Gly His Val Met Glu  
 245 250 255  
 Gly Ser Pro Thr Gly Thr Thr Val Met Arg Met Thr Ala Phe Asp Ala  
 260 265 270  
 Asp Asp Pro Ala Thr Asp Asn Ala Leu Trp Arg Tyr Asn Ile Arg Gln  
 275 280 285  
 Gln Thr Pro Asp Lys Pro Ser Pro Asn Met Phe Tyr Ile Asp Pro Glu  
 290 295 300  
 Lys Gly Asp Ile Val Thr Val Val Ser Pro Ala Leu Leu Asp Arg Glu

305		310		315		320
Thr Leu Glu Asn Pro Lys Tyr Glu Leu Ile Ile Glu Ala Gln Asp Met						
		325		330		335
Ala Gly Leu Asp Val Gly Leu Thr Gly Thr Ala Thr Ala Thr Ile Val						
		340		345		350
Ile Asp Asp Lys Asn Asp His Ser Pro Lys Phe Thr Lys Lys Glu Phe						
		355		360		365
Gln Ala Arg Val Glu Glu Gly Ala Val Gly Val Ile Val Asn Leu Thr						
		370		375		380
Val Glu Asp Lys Asp Asp Pro Thr Thr Gly Ala Trp Arg Ala Ala Tyr						
		385		390		400
Thr Ile Ile Asn Gly Asn Pro Gly Gln Ser Phe Glu Ile His Thr Asn						
		405		410		415
Pro Gln Thr Asn Glu Gly Met Leu Ser Val Val Lys Pro Leu Asp Tyr						
		420		425		430
Glu Ile Ser Ala Phe His Thr Leu Leu Ile Lys Val Glu Asn Glu Asp						
		435		440		445
Pro Leu Val Pro Asp Val Ser Tyr Gly Pro Ser Ser Thr Ala Thr Val						
		450		455		460
His Ile Thr Val Leu Asp Val Asn Glu Gly Pro Val Phe Tyr Pro Asp						
		465		470		475
Pro Met Met Val Thr Lys Gln Glu Asn Ile Ser Val Gly Ser Val Leu						
		485		490		495
Leu Thr Val Asn Ala Thr Asp Pro Asp Ser Leu Gln His Gln Thr Ile						
		500		505		510
Arg Tyr Ser Ile Tyr Lys Asp Pro Ala Gly Trp Leu Ser Ile Asn Pro						
		515		520		525
Ile Asn Gly Thr Val Asp Thr Thr Ala Val Leu Asp Arg Glu Ser Pro						
		530		535		540
Phe Val His Asn Ser Val Tyr Thr Ala Leu Phe Leu Ala Ile Asp Ser						
		545		550		555
Gly Asn Pro Pro Ala Thr Gly Thr Gly Thr Leu Leu Ile Thr Leu Glu						
		565		570		575
Asp Ile Asn Asp Asn Ala Pro Val Ile Tyr Pro Thr Val Ala Glu Val						
		580		585		590
Cys Asp Asp Ala Arg Asn Leu Ser Val Val Ile Leu Gly Ala Ser Asp						
		595		600		605
Lys Asp Leu His Pro Asn Thr Asp Pro Phe Lys Phe Glu Ile His Lys						
		610		615		620



Gln Thr Val Pro Asp Lys Val Trp Lys Ile Ser Lys Ile Asn Asn Thr  
 625 630 635 640  
 His Ala Leu Val Ser Leu Leu Gln Asn Leu Asn Lys Ala Asn Tyr Asn  
 645 650 655  
 Leu Pro Ile Met Val Thr Asp Ser Gly Lys Pro Pro Met Thr Asn Ile  
 660 665 670  
 Thr Asp Leu Lys Val Gln Val Cys Ser Cys Lys Asn Ser Lys Val Asp  
 675 680 685  
 Cys Asn Gly Ala Gly Ala Leu His Leu Ser Leu Ser Leu Leu Leu Leu  
 690 695 700  
 Phe Ser Leu Leu Ser Leu Leu Ser Gly Leu  
 705 710

<210> 5  
 <211> 36  
 <212> DNA  
 <213> Artificial

<220>  
 <223> primer

<400> 5  
 aagaattccg ccaccatgct actgttgcaa gctctc

36

<210> 6  
 <211> 45  
 <212> DNA  
 <213> Artificial

<220>  
 <223> primer

<400> 6  
 gactacaagg acgacgatga caaggaagat gacgttacta caact

45

<210> 7  
 <211> 45  
 <212> DNA  
 <213> Artificial

<220>  
 <223> primer

<400> 7  
 cttgtcatcg tcgtccttgt agtcggcatg actgggcagg attaa

45

<210> 8  
 <211> 30  
 <212> DNA

<213> Artificial

<220>

<223> primer

<400> 8

tttgaattct cagttggtat catggttagag

30

<210> 9

<211> 36

<212> DNA

<213> Artificial

<220>

<223> primer

<400> 9

aagaattccg ccaccatgct actgttgcaa gctctc

36

<210> 10

<211> 60

<212> DNA

<213> Artificial

<220>

<223> primer

<400> 10

tttgaattct cacttgctgt catcgtcttt gtagtctgca cttgcatcgt tggatatcatg

60

<210> 11

<211> 18

<212> DNA

<213> Artificial

<220>

<223> primer

<400> 11

gacatctcct gtcccaag

18

<210> 12

<211> 18

<212> DNA

<213> Artificial

<220>

<223> primer

<400> 12

ctaacatggt ctacatcg

18

<210> 13

<211> 18

<212> DNA  
<213> Artificial  
  
<220>  
<223> primer  
  
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ctgtccacat cacagtcc

18

<210> 14  
<211> 19  
<212> DNA  
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<223> primer  
  
<400> 14  
cagacagtcc ctgataaag

19

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<211> 20  
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<223> primer  
  
<400> 15  
ctcgttgccc ttgcagtcac

20

<210> 16  
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<212> DNA  
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<223> primer  
  
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gacttccaga ggcactggc

19

<210> 17  
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ggctcctgtg gtgggggtcg

19

<210> 18

12

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ggttgccact gtcgatgg

18